

GGCTGAGGGGAGGCCCGGAGGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA
GAGAAGCGCCTGCAGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAA
AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC
CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGA
AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCT
CTGTGGAGGCAGAGCCAGTGGAGCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCA
ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATG
TGAGGAGCCGCCCGGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
ATAACCACCATTTTTGCAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTTGAGGGCACTGAGGAGGGCTC
GCCAAGAGAGTTTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCA
CCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAG
CCTGAGGTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT
GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG
TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTACGCGAGCTC
TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACCGGTTGGAGCTCTCCCAGCT
GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATCGCGCAG
CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCCCCCGCTGC
CCCCCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG
AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCCACTATGCCCCACTCTC
ACCAGCCTCCCATCTTCCACCGACAAGCCGTGCGGGCCCATGGAGAGACTGCCTGCAGGCCCT
GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCA
TGCAGGTGTGGTGCGACCAGAGACAGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTG
GATGGCTCTGTTAACTTCTTCAGGAACTGGGAGACGTACAAGCAAGGGTTTGGAACATTGA
CGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC
TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGCAGAATACGCCAGTTTCCGC
CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA
CTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCTGGACAGAGATCATGATGTCTACA
CAGGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC
CTCAACGGGGTCTGGTACC GCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTG
GGCTGAGTTCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGATCCGACCGAACC
CCAACACCTTCCACTAAAGCCAGCTCCCCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCA
CCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTCATCCTGAGGCTGGGA
GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGAT
ACGGTGTTTTCTGTCCCTCCTACTTTCTTTCACACCAGACAGCCCTCATGTCTCCAGGACA
GGACAGGACTACAGACAACCTCTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAAA

FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
Q RVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHCQRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFFRNWETYSKQGFNGNIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNAHYQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH
```

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479

Amidation site.

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCGGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
GTTCCCTCTTTCCGGGGGTCTCACCAGAAGAGGTTCTTGGGGGTGCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAATTC
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCCGGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCAGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ

AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDLAVIRTLVDK

Important features:**Signal peptide:**

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAACAAGTTAAATGTCTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
G**TAG**CCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAACAAACAGG
CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVFESRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDDSTYTLFNLIIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELEFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 7

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
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><subunit 1 of 1, 247 aa, 1 stop
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><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGI VTRLYCRQGYLQMHPDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

CTCGCAGCCGAGCGCGGCCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCA
GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCACT
GTGTCCAGACTGAGGCCCCATTTGCATTGTTTAACATACTTAGAAAATGAAGTGTTCATTTT
TAACATTCTCTCTCCAATTGGTTTAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGT
GCTTGCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCTCTCCA
CGACTCGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGGCCGA
CGTGCCCGAGCTCCTCCGGGGGTCCCGCCCGGAGCTTTCTTCTCGCCTTCGCATCTCCTC
TCGCGCGTCTTGACATGCCAGGAATAAAAAGGATACTACTGTTACCATTCTGGCTCTCTG
TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
CAGGACAGTGTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATG
ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCCTGTGTATCGAGG
GCCCTACTCGAACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCAC
TCTCAGCTCCAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATAACAGATG
GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCC
CACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGC
TTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTGCTATGGTTACTGCCAGCAGCTCTGT
GCGAATGTTCTTGATCCTATTCTTGTACATGCAACCCCTGGTTTTACCCTCAATGAGGATGG
AAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCCTGCGTGCAAACCTGCGTCA
ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTT
CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAA
CCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAA
GCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC
TACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG
GATCAGTGATAACCGCTGTATGTGTCTGTGTGAGAACCCTGGCTGCAGAGACCAGCCCTTTA
CCATCTTGTACCGGGACATGGACGTGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAA
ATGCAAGCCACGACCCGCTACCCCTGGGGCCTATTACATTTTCCAGATCAAATCTGGGAATGA
GGGCAGAGAATTTTACATGCGGCAAACGGGGCCCATCAGTGCCACCCCTGGTGATGACACGCC
CCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGAAATGATCACTGTCAACACTGTCTATC
AACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGCGAGTACCCATTCTGAGC
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GTCAGCCCCGACTTCTGACTCTCACCTGTACTATTGCAGACCTGTACCCTGCAGGACTTG
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TTGTTGGTGAATTTTCAAGGCCTTCAGTTTATTTCCACTATTTTCAAAGAAAATAGATTAGG
TTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGTGAACAGCTTGCTGTCACTTCTTCACCTC
TTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGGAACCCCT
GGGAGTAGCTAGTTTGGCTTTTTGCGTACACAGAGAAGGCTATGTAAACAAACCACAGCAGGA
TCGAAGGGTTTTTAGAGAATGTGTTTTCAAACCATGCCTGGTATTTTCAACCATAAAAGAAG
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AAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCC
AAACCCAGTCTCCTCTCCATTTTAGCCCAGTGTTTTCTTTGAGGACCCCTTAATCTTGCTTT
CTTTAGAATTTTTTACCCAATTGGATTGGAATGCAGAGGTCTCCAAACTGATTAAATATTTGA
AGAGA

FIGURE 10

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQ
CVDVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQQLCANVPG
SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSGLICRCDPGYELEEDGVHCSDM
DECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG
GFKCIDPIRCEEPLYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATT
RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGS
SVIRLRIYVSOYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

FIGURE 11

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCACGCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTG
 GAAGGAGGGAGTGCGCGGGCTGCCCCGGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTT
 CCAGGCACCCTGTCTGGGGCAGGGAGGGCACAGGCCTGCACATCGAAGGTGGGGTGGGACCA
 GGCTGCCCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCGTGGCCCTGCAGACTCTCA
 GGGCTAAGGTCTCTGTTGCTTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT
 AGCTTGAAGGAGGCACCATGCAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTG
 GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTG
 TGCCTACCGCGACCTAGAATCCGTGCCGCTGGCTTCCCGGCCAATGTGACTACACTGAGCC
 TGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCAGGGAGGTGCCCTGCTGCAG
 TCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGAGCCCTGGCCTCTCTGAG
 CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGC
 ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC
 GACGCCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGCACAC
 ATTGGCCGAGGGCACCTTCACCCCGCTCACCGCGCTGTCCACCTGCAGATCAACGAGAACC
 CTTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCGTGTCC
 ATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGCTGAG
 CCGCCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGG
 ATGGTGCCGAGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCG
 GCCCCCTCAGCTTCACTGGCACATCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAA
 CGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCCAGCTCCCAGCCGCGCTTCC
 AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
 AGCTGCCTGGCCACCAATGAGCTGGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCCAC
 GCCCCGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAA
 AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATC
 ATCTACCTCAGCCGTGCTGGGAACCCTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCT
 GCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTTCTTCTTCTCCTCACCTCCTTCTT
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 CAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCCTACCTCT
 CTTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAAACTAGTGA
 CTAGGATAGAATTTGATCCCCTAACTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTG
 CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCTAATCCAACCTGGGAGAA
 GCCTCAGTGGTGGAATTCCAGGCACTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA
 ATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGGATGG
 GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCT
 CTTTGCTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAA
 TGTGGGGATCCAGGATGGCCTTCCTTCCTCTTACCCTTCCTCCCTCAGCCTGCAACCTCTAT
 CCTGGAACCTGTCCTCCCTTTCTCCCCAACTATGCATCTGTTGTCTGCTCCTCTGCAAAGGC
 CAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAAA
 AAGGGCGGCCGCGACTCTAGAGTCGACCT

FIGURE 13

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC
 AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTCCCGGC
 AGCGAGGAGGTCCTGAGCAGCATGGCCCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT
 CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCGCAGGAGGAGA
 GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
 CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAG
 AATGCCAGCTATTCCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
 CAGAATACTTCTATGAATTCCTGTCCTTGCGCTCCCTGGATAAAGGCATCATGGCAGATCCA
 ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT
 CCCATGTCTTGGAACAGGATGGGGTGGCAGCATTGAAAGTGGATGTGATTGTTATGAATT
 CTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATGTCAACAA
 GCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG
 TCCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG
 GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAACGTG
 GACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCCTGGAAAATG
 TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCACAACCCTGTC
 GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGGAGAC
 CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA
 CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
 TCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG
 GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACTCCGACATCTGAAAC
 GTTTTAAGTTACACCAAGTTCATAGCCTTTGTAAACCTTTCATGTGTTGAATGTTCAAATAA
 TGTTTCATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
 GATATTTACTCTTCCTTTTAAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT
 TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTAAATTTTCAGTG
 TGTAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT
 CAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT
 TGAAGTTACAGCATTTTCAAGTTTTATTGTCAGATATTTAGATGTTTGTTACATTTTAAAAA
 TTGCTCTTAATTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCAGAGATT
 CAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTAAACAATATAATATATTCTA
 AACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATA
 TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT
 AAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESESLYLWIDAHQARVLIGFEEDILIVSEGK
 MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
 GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGC
 RGGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
 TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCKGSKCKCSKGYQGDLCSPVC
 EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHPSLKKAEERRDP
 PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.5	2.5	9	16
Occupation	1.8	0.8	1	4
Income	1.5	0.5	1	3
Health status	1.2	0.4	1	2
Stress level	2.5	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work-life balance	2.8	1.2	1	4
Family support	1.8	0.8	1	3
Community involvement	1.5	0.5	1	3
Volunteer work	1.2	0.4	1	2
Charitable contributions	1.0	0.3	1	2
Philanthropic activities	1.1	0.4	1	2
Environmental activism	1.3	0.5	1	2
Animal welfare work	1.4	0.6	1	2
Human rights advocacy	1.5	0.7	1	2
Peacekeeping efforts	1.6	0.8	1	2
Disaster relief work	1.7	0.9	1	2
Public health initiatives	1.8	1.0	1	2
Education reform projects	1.9	1.1	1	2
Arts and culture programs	2.0	1.2	1	2
Sports and recreation activities	2.1	1.3	1	2
Community development projects	2.2	1.4	1	2
Urban planning initiatives	2.3	1.5	1	2
Infrastructure improvement projects	2.4	1.6	1	2
Public safety programs	2.5	1.7	1	2
Law enforcement initiatives	2.6	1.8	1	2
Fire department projects	2.7	1.9	1	2
Emergency services programs	2.8	2.0	1	2
Public works projects	2.9	2.1	1	2
Infrastructure development projects	3.0	2.2	1	2
Urban renewal projects	3.1	2.3	1	2
Public housing projects	3.2	2.4	1	2
Community centers	3.3	2.5	1	2
Public libraries	3.4	2.6	1	2
Community gardens	3.5	2.7	1	2
Public art projects	3.6	2.8	1	2
Historical preservation projects	3.7	2.9	1	2
Archaeological excavations	3.8	3.0	1	2
Museum projects	3.9	3.1	1	2
Historical research projects	4.0	3.2	1	2
Architectural projects	4.1	3.3	1	2
Urban design projects	4.2	3.4	1	2
Public space projects	4.3	3.5	1	2
Public transit projects	4.4	3.6	1	2
Public transportation projects	4.5	3.7	1	2
Public works projects	4.6	3.8	1	2
Infrastructure projects	4.7	3.9	1	2
Urban development projects	4.8	4.0	1	2
Public housing projects	4.9	4.1	1	2
Community centers	5.0	4.2	1	2
Public libraries	5.1	4.3	1	2
Community gardens	5.2	4.4	1	2
Public art projects	5.3	4.5	1	2
Historical preservation projects	5.4	4.6	1	2
Archaeological excavations	5.5	4.7	1	2
Museum projects	5.6	4.8	1	2
Historical research projects	5.7	4.9	1	2
Architectural projects	5.8	5.0	1	2
Urban design projects	5.9	5.1	1	2
Public space projects	6.0	5.2	1	2
Public transit projects	6.1	5.3	1	2
Public transportation projects	6.2	5.4	1	2
Public works projects	6.3	5.5	1	2
Infrastructure projects	6.4	5.6	1	2
Urban development projects	6.5	5.7	1	2
Public housing projects	6.6	5.8	1	2
Community centers	6.7	5.9	1	2
Public libraries	6.8	6.0	1	2
Community gardens	6.9	6.1	1	2
Public art projects	7.0	6.2	1	2
Historical preservation projects	7.1	6.3	1	2
Archaeological excavations	7.2	6.4	1	2
Museum projects	7.3	6.5	1	2
Historical research projects	7.4	6.6	1	2
Architectural projects	7.5	6.7	1	2
Urban design projects	7.6	6.8	1	2
Public space projects	7.7	6.9	1	2
Public transit projects	7.8	7.0	1	2
Public transportation projects	7.9	7.1	1	2
Public works projects	8.0	7.2	1	2
Infrastructure projects	8.1	7.3	1	2
Urban development projects</				

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.5	2.5	9	16
Occupation	1.8	0.8	1	4
Income	1.5	0.5	1	3
Health status	1.2	0.4	1	2
Stress level	2.5	1.5	1	5
Life satisfaction	3.5	1.5	1	5
Work-life balance	2.8	1.2	1	4
Family support	1.8	0.8	1	3
Community involvement	1.5	0.5	1	3
Volunteer work	1.2	0.4	1	2
Charitable donations	1.0	0.3	1	2
Political participation	1.5	0.5	1	3
Civic engagement	1.8	0.8	1	3
Environmental awareness	1.5	0.5	1	3
Social media usage	2.5	1.5	1	5
Online shopping	3.5	1.5	1	5
Smartphone usage	4.5	1.5	1	5
Internet usage	4.8	1.5	1	5
Video streaming	4.2	1.5	1	5
Online gaming	3.8	1.5	1	5
Cloud storage	3.5	1.5	1	5
Mobile banking	3.2	1.5	1	5
Online news	3.0	1.5	1	5
Online education	2.8	1.5	1	5
Online healthcare	2.5	1.5	1	5
Online shopping	2.2	1.5	1	5
Online banking	2.0	1.5	1	5
Online news	1.8	1.5	1	5
Online education	1.5	1.5	1	5
Online healthcare	1.2	1.5	1	5
Online shopping	1.0	1.5	1	5
Online banking	0.8	1.5	1	5
Online news	0.5	1.5	1	5
Online education	0.2	1.5	1	5
Online healthcare	0.0	1.5	1	5
Online shopping	-0.2	1.5	1	5
Online banking	-0.5	1.5	1	5
Online news	-0.8	1.5	1	5
Online education	-1.0	1.5	1	5
Online healthcare	-1.2	1.5	1	5
Online shopping	-1.5	1.5	1	5
Online banking	-1.8	1.5	1	5
Online news	-2.0	1.5	1	5
Online education	-2.2	1.5	1	5
Online healthcare	-2.5	1.5	1	5
Online shopping	-2.8	1.5	1	5
Online banking	-3.0	1.5	1	5
Online news	-3.2	1.5	1	5
Online education	-3.5	1.5	1	5
Online healthcare	-3.8	1.5	1	5
Online shopping	-4.0	1.5	1	5
Online banking	-4.2	1.5	1	5
Online news	-4.5	1.5	1	5
Online education	-4.8	1.5	1	5
Online healthcare	-5.0	1.5	1	5
Online shopping	-5.2	1.5	1	5
Online banking	-5.5	1.5	1	5
Online news	-5.8	1.5	1	5
Online education	-6.0	1.5	1	5
Online healthcare	-6.2	1.5	1	5
Online shopping	-6.5	1.5	1	5
Online banking	-6.8	1.5	1	5
Online news	-7.0	1.5	1	5
Online education	-7.2	1.5	1	5
Online healthcare	-7.5	1.5	1	5
Online shopping	-7.8	1.5	1	5
Online banking	-8.0	1.5	1	5
Online news	-8.2	1.5	1	5
Online education	-8.5	1.5	1	5
Online healthcare	-8.8	1.5	1	5
Online shopping	-9.0	1.5	1	5
Online banking	-9.2	1.5	1	5
Online news	-9.5	1.5	1	5
Online education	-9.8	1.5	1	5
Online healthcare	-10.0	1.5	1	5
Online shopping	-10.2	1.5	1	5
Online banking	-10.5	1.5	1	5
Online news	-10.8	1.5	1	5
Online education	-11.0	1.5	1	5
Online healthcare	-11.2	1.5	1	5
Online shopping	-11.5	1.5	1	5
Online banking	-11.8	1.5	1	5
Online news	-12.0	1.5		

FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

CGGAGAACCTTTGCGACGCGACAAACTACGGGGACGATTCTCTGATTGATTTTTTGGCGCTTTCGATCCACCCCTCC
TCCCTTCTC**AT**GGGACTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC
CAGGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCGTCTTCATCGTCGCGG
TTCTGCTGCCGTCCGGGTGACTCTGCCACCATCCCCGGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTG
TAACCCGTGCACAGAGGGTGTGGATTACACCATTGTCTCCAACAATTTGCCTTCTTGCTGCTATGTACAGTTT
GTAAATCAGGTCAAACAAATAAAGATTCTCTTACCACGACAGACACCGTGTGTCAAGTGTGAAAAGGAAGC
TTCCAGGATAAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCCAGAGGATGGTCAAGGTCAG
TAATTGTACGCCCCGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAACCCAGCAG
CGGAGGAGACAGTGACCACCATCTCGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTA
GTCATCATTTTAGCTGTGGTTGTGGTTGGCTTTTCATGTGCGGAAGAAATTCATTTCTTACCTCAAAGGCATCTG
CTCAGGTGGTGAGGAGGTCCCGAACGTGTGCACAGAGTCTTTTCCGGCGCGTTCATGCTCTTACAGAGTTT
CTGGGGCGGAGGACAATTGCCGCAACGAGACCTGAGTAACAGATACTTGACGCCACCCAGGTCTCTGAGCAG
GAAATCCAAGGTCAAGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGACTCGCCAGAGGAGCCACAGCGTCTGCT
GGAACAGGCAGAAGCTGAAGGGTGTGAGGAGGAGGCTGCTGGTTCAGTGAATGACGCTGACTCCGCTGACA
TCAGCACCTTGCTGGATGCTCGGCAACACTGGAAGAAGGACATGCAAGGAACAATTACAGGACCAACTGGTG
GGCTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCTG**TGA**AAGAATCTCTTCAG
GAACACGAGCTCTCCCTCATTTACCTTTCTCTCTCAAAAGGGAAGCAGCTGGAAGAAACAGTCCAGTACTTGA
CCCATGCGCCAAACAACCTCTACTATCCAATATGGGGCAGCTTACCAATGGTCTAGAACTTTGTTAACGCACCT
GGAGTAATTTTTTATGAAATACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGT
TATACGATTGTGTATTAAGGGTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCAGCACTTTGATAG
GCTGAGGCAGGTGGATTGCTTGAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAAT
TTAAAAAGAAAAAAGTGGTTTTAGGATGTCATTCTTTGCAGTTCCTTCATCATGAGACAAGTCTTTTTTTCTGC
TTCTTATATTGCAAGCTCCATCTCTACTGGTGTGTGCATTATGACATCTAACTACAGATGCCGCACAGCCAC
AATCGATTTTGCCTTATAGTTTTTAACTTTAGAGCGGATTACTTGTATTACTTCCCTGATTTTTCAGTTTCGGATA
TTTTTGACTTAATGATGAGATTATCAAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTC
GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTG
CTTACTACTGTAGGCTGTACATCTCTTTTCCGATTTTTGTATAATGATGTAAACATGGAAAACTTTAGGAAAT
GCACATTATTAGGCTGTTTACATGGGTTGCCTGATACAAATCAGCAGTCAAAAATGACTAAAAATAAACTAGT
GACGGAGGGAGAAATCCTCCCTCTGTGGAGGCACTTACTGCATTCAGTTCCAGTTCTCCCTCCTGCGCCCTGAGACTG
GACCAGGGTTTGATGGCTGGCAGCTTCTCAAGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCA
TATTTATTTATAAATAAATATTTATTTATTTATTTATAAGTAGATGTTTACATATGCCCAGGATTTTGAAGAGC
CTGATATCTTTGGGAAGCATGTGTCTGGTTTGTCTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGT
CACAGCAGATGAGGACAGTGAGAATTAAAGTTAGATCCGAGAGTCGGAAGAGCTTCTCTTTCAAGCGCCATTACA
GTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCC
ATGGCATCAAGAGGGAAGAGTGGACGCTTGTTGGGAATGGTGTGAAATGGTTGCCACTCAGGCATGGATGGGC
CCCTCTCGCTTCTGGTGGTCTGTGAACTGAGTCCCTGGGATGCCTTTTAGGGCAGAGATTCTGAGCTGCGTTT
TAGGGTACAGATTCCCTGTTTGAAGGAGCTTGGCCCTCTGTAAGCATCTGACTCATCTCAGAGATATCAATTCT
TAAACACTGTGACAACGGGATCTAAAATGGCTGACACATTTGTCTTGTGTACGTTCCATTATTTTATTTAAA
AACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACTCTTCTCCACAGTAGCCAGTCGTGGTAGGATAAAATTA
CGGATATAGTCATTTAGGGTTTTCAGTCTTTCCATCTCAAGGCATTGTGTGTTTGTTCGGGACTGGTTG
GCTGGGACAAAGTTAGAAGTGCCTGAAGTTCGCACATTCAGATTGTTGTGTCCATGAGGATTTAGGAGGGATG
GCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATCTGGCGTCCACACCTTGTCCCCTGCACCTCTG
GATGACACAGGGTGTGCTGCCTCCTAGTCTTTGCTCTTGTGGGCTTCTGTGCAGGAGACTTGGTCTCAAAG
CTCAGAGAGAGCCAGTCCGTCCTCAGCTCCTTTGTCCCTTCTCAGAGGCCTTCTTGAAGATGCATCTAGACT
ACGACCTTATCAGTGTTTAAAGCTTATCTCTTAAACATAAGCTTCTTGACAACATGAAATTTGTTGGGGTTTTT
GGCGTTGGTTGATTGTTTGGTTTGGTTTCTTTAATCCCGGCCAAATAGCACATAACACCTGGTTATATATGAAA
TACTCATATGTTTATGACCAAAATAAATATAAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD
EVPQQT VAPQQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
QTNKSSCTTTTRDTVCQCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAA
SSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIIILAVVVVGFSCRKKFISYLKGICSGGG
GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAELTGVTVES
PEEPQRLLEQAEAEGCQRRRLLVPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKL
FYEEDEAGSATSCL

Important features of the protein:

Transmembrane domains:

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

FIGURE 19

GCGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAAGTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCCTTAAAAA

FIGURE 20

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FIGURE 21

CCGGGGAGGGGAGGGCCCCGTCCCGCCCCTCCCCGTCTCTCCCCGCCCCTCCCCGTCCCTCCC
GCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGCTGCCCTC
TGCCCGGGTTGTCCAAGATGGAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG
TTCGTGGCGCTACCCGCCTCCGGCTGGCTGACGACGGGCGCCCCGAGCCGCCGCGCTGTC
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAAC TACACTGAAAGATGATGGGGACATAT
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA
CCTGTAAATAGTGGTGTAACCCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT
TGAAAATTTGGAGGAAAAAGAATATTTTGGAAATTGTCAGTGTAAGGATTTTAGTTCATGAGT
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
GATGGAAAACAAGTTCAGCAAAAGGATGTCACTGAAATTGATATTTTAGTTAAGAACCGGGG
AGTACTCAGACATTCAAAC TATAACCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC
GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCCAAAAAAGAAAGTGTTAGTTCACTG
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTTACC
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
AAAGGTGTTTTTTCCAGTTTCTGAATACAAAGGAATTCTTCAGTTGGATAAAGTGGACGTCA
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
GATAAAACATGTATTTAAAACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783

><subunit 1 of 1, 330 aa, 1 stop

><MW: 36840, pI: 4.84, NX(S/T): 4

MEGAPPGSLALRLLLEFVALPASGWLTGGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQQKDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRDSIL
FTLPNLSKKESVSSLQTTSQYLIRNVETTVDVLPGLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAADVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPEKRAENLEDKTCI

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

CGTCTCTGCGTTTCGCCATGCGTCCCAGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGG
CCCTGGCTTTGGGCGGTGGGCTTCTGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGT
GTTTGTCTGGCTCCAGCAGGGCGCCAGGAGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCAC
CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG
GGAACAAGATCAACCTCCTCGGCTTCTTGGGCGCTTGTCCACTGCCTTCCCTGCAAAGATTTCG
TGCAGCGGCGTGGAGTGCGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGCTG
CGAGTGC CGCGCCGACTGCTCGGGGCTCCC GGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG
CCACCTACCGCGACGAGTGCAGACTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGC
GTCATGTACCGGGGCCGCTGCCGCAAGTCCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTC
GTGCGTCTGTGGACCAGACGGGCGAGCGCCCACTGCGTGGTGTGTGCGAGCGGCGCCCTGCCCTG
TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGC
CACATGCGCCAGGCCACCTGCTTCTTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG
CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAAGTTCGTGT
GAGCCTGCAGGACAGGCCTGGGCGCTGGTGCCGAGGCCCCCATCATCCCCTGTTATTTATT
GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTT
GGGGATCCCAGAACCTCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGGCC
GGCTGGTGGGTGGGATAGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT
AGGATGCCCCAGCCCCCTACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTT
TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATT
CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT
CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG
TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG
CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGGCGTGTGGGGA
CCTCAGAACACTGTGACCTTAGCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC
CACCATTCCCTGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
CCTGTGAAGGCCATTGAGAAATGCCAGTGTGCCCTTGGGAAAGGGCACGGCCTGTGCTCC
TGACACGGGCTGTGCTTGGGCCAGAACCAAGCCAGCGTCTCCCCTGCTGCTGTCCACGTCAG
TTCATGAGGCAACGTGCGCTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGC
ACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGACCACGGGCCACTGC
TACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT
CCTGGAGCCGGGTGTCCAGTGGCACCACCTAGGTGCCTGCTGCCTCCACAGTGGGGTTCACA
CCCAGGGCTCCTTGGTCCCCCACAACCTGCCCCGGCCAGGCCTGCAGACCCAGACTCCAGCC
AGACCTGCCTCACCCACCAATGCAGCCGGGGCTGGCGACACCAGCCAGGTGCTGGTCTTGGG
CCAGTTCTCCCACGACGGCTCACCCCTCCCCTCCATCTGCGTTGATGCTCAGAATCGCCTACC
TGTGCCTGCGTGTA AACACAGCCTCAGACCAGCTATGGGGAGAGGACAACACGGAGGATAT
CCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCCTCCTCCAGCCTCCTC
CAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCAGAAAAGTGCCCTAGGTTGGTGGGTCTA
CAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCCCTGCCTCACCAAGGAAATAAAGA
CTCAAGCCATAAAAAAAAAA

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGVSSMSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVECGPGKACRMLGGRPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCEHVVCPRPQSCVVDQ
TGSAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCTGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGT
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT
AAAATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAA
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCGCCTGGCTA
CCATGATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTTCATCCATCCTTTAAATCTG
CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACT
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA
TTAAATTAGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTG
TTAGACAAGTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGA
AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGAATGCTTAATCGAACACTTCTTG
AAACCTTGCAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCCTG
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGC
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC
AAGTACACAGGAAATCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAACAGAGACTCG
TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTA
CTTTTCTCAACTTTGATCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACA
ACTTTAGTTAAGGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGG
CCTTAATACAGTTTTAACCCTGATAATTCAGATTTGTTCATTAACAGTATTGGGATTGTGC
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATC
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTTCTGTCCTATGATTATGC
TGTGAAGAAGCCATGGCTTGCATATCCTCACTATAAGCCCCCGGAGAAATGCCCCCTCTATCA
TTCTCCATGATCGACTTTATTACCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATG
AGTGCCATTGCAGCCCACAACGCTGCACTCCTTGCCTATCACCGCTGGAACGGGCACACAGA
CATGATTGATCAGGATGGCTTATATGAGAACTTAAACTGAACTATTGAAGTGACACACTCC
TTTTTCCCCTCCTAGTTCCAAATGACTATCAGTGGCAAAAAGAACAAAATCTGAGCAGAGA
TGATTTTGAACCAGATATTTTGCCATTATCATTTGTTTAATAAAAGTAATCCCTGCTGGTCAT
AGGAAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDKIAIIGAGIGGTSAAYYLRQKFGKDVK
IDLFEREEVGGRLATMMVQGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGE
TLVFEESNWFIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL
GGDDFLGMLNRTLLETLOKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLW
AVEGGNKLVCSSLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDI
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGNLTVLT
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTQAQILKLFLSYDYAVKKPWL
AYPHYKPPEKCPSSIILHDLRYLLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDG
LYEKLKTEL

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

FIGURE 27

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGAC**ATGAT**
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCAGTCAGAGCTA**TAA**
GAGATGATGGAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAATCTGA

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQSKKPL
MVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation site.

amino acids 51-57

FIGURE 29

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCAC
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9700, pI: 9.55, NX(S/T): 0

MKKVLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFP
WFRRNFPIPIPIESAPTTPLPSEK

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

protein "B3-hordein"

CGGACGCGCTGGGCGGGCGCGCCGGGAGGAGGACCGGCGGCGGCGCATGGCGCCGGGGGGCCCTGGGAT
GCGGGCCCCGTCTCGCCGCCTGCTGCCGCTGTTGCTGCTGCTCGGCCCTGGCCCGCGCGCGCCGC
GGGAGCGCCGGGCCCCGACGGTTTAGACGTCTGTGCCACTTGCCATGAACATGCCACATGCC
AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTTGTAGGGAACGGGAGGACT
CAGTGTGTTGATAAAAAATGAGTGCCAGTTTGGAGCCACTCTTGTCTGTGGGAACACACATC
TTGCCACAACACCCCCGGGGGCTTCTATTGCATTTGCCTGGAAGGATATCGAGCCACAAACA
ACAACAAGACATTCATTCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT
TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG
TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCACCGATGCCACAT
CATGCACAGAAATAGACTGTGGTACCCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT
TATACGTCTAGTCTGGGCAGCCAGGTTTCGTTATGCTTGCAGAGAAGGATTCTTCAGTGTTC
AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC
AAGAGATCAACTGTGGCAACCCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAGC
TCCAGGCTGGGCGGTGTGGCTCGCTATGTCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA
GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAACATGCACAGAAA
TTCTGACAAAGATTAATGATGTATCACTGTTTAATGATACCTGTGTGAGATGGCAAATAAAC
TCAAGAAGAATAAACCCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC
TATGGAATCAGTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCAGAGTGT
GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAACATCTCCACAGCACCTCCCAGGCGC
TCGATGCCAGCCGTCAATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG
TTTCAATATTTCAATATTTAATGAACTTGTTTGAAATTGAACAGGCGTTCTAGGAAAGTTG
GATCAGAACACATGTACCAATTTACCGTTCTGGGTGAGAGGTGGTATCTGGCTAACTTTTCT
CATGCAACATCGTTTTAACTTCACAACGAGGGAACAAGTGCCTGTAGTGTGTTTGGATCTGTA
CCCTACGACTGATTATACGGTGAATGTGACCCTGCTGAGATCTCCTAAGCGGCACTCAGTGC
AAATAACAATAGCAACTCCCCCAGCAGTAAAACAGACCATCAGTAACATTTTCAGGATTTAAT
GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTATTTATTTCCA
CATTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCCAGGAAATGACCTTTAATATCAGTA
GCAGCAGCCGAGATCCCGAGGTGTGCTTGGACCTACGTCCGGGTACCAACTACAATGTCAGT
CTCCGGGCTCTGTCTTCGGAACCTTCCTGTGGTCATCTCCCTGACAACCCAGATAACAGAGCC
TCCCCTCCCGGAAGTAGAATTTTTTTACGGTGCACAGAGGACCTCTACCACGCTCAGACTGA
GGAAAGCCAAGGAGAAAAATGGACCAATCAGTTCATATCAGGTGTTAGTGTCTCCCTGGCC
CTCCAAAGCACATTTTCTTGTGATTCTGAAGGCGCTTCCTCCTTCTTTAGCAACGCCTCTGA
TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA
TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGCACCCTTGAAAAGAGGGAGT
GATTACTGCATTATATTACGAATCACAAGTGAATGGAATAAGGTGAGAAGACACTCTCTGTGC
AGTTTGGGCTCAGGTGAAAGATTTCGTCACTCATGCTGCTGCAGATGGCGGGTGTGGACTGG
GTTCCCTGGCTGTTGTGATCATTCTCACATTCTCTCCTTCTCAGCGGTGATGGCAGATG
GACACTGAGTGGGGAGGATGCACTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCCC
GCACAGAGGCTCCGTGTGACTTCCGTCCAGGGAGCATGTGGGCCTGCAACTTTCTCCATTCC
CAGCTGGGCCCCATTTCCTGGATTTAAGATGGTGGCTATCCCTGAGGAGTCACCATAAGGAGA
AAACTCAGGAATTCTGAGTCTTCCCTGCTACAGGACCAGTTCTGTGCAATGAACTTGAGACT
CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC
TTCTCTGAGTGTGCTGAGGGTCAGCTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA
ACCTCCTATATAAAAGCATTTTCTGTTAATTCATTTCAGAATCCATTCTTTACAATATGCAGTG
AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTTCATTGAAAAAGAGAAC
GTGACGTAGGCAAATGTTTCAAGCACTTTAGAAACAGTACTTTTCTATAATTAGTTGATAT
ACTAATGAGAAAAATATACTAGCCTGGCCATGCCAATAAGTTTCCCTGCTGTGTCTGTTAGGCA
GCATTGCTTTGATGCAATTTCTATTGTCTTATATTCAAAGTAATGTCTACATTCCAGTA
AAAATATCCCGTAATTAATAA

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPSRRLPLLLLLLGLARGAAGAPGPDGLDVCATCHEHATCQQREGKKICICNYG
FVGNGRQTQCVDKNECQFGATLVCGNHTSCHNTPGGFYCICLEGYRATNNNKTFIPNDGTFTCT
DIDECEVSGLCRHGGRCVNTHGSEFCYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPPEVP
DGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTWESPCLHCQEINCGNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFESPGGKITSVCTEKG TWRESTLTCTEILT KINDVSLFNDT
CVRWQINSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVCLALYPGTNYTVNI
STAPRRSMPAVIGFQTAEVDLLEDDGSFNISIFNETCLKLNRRSRKVGSEHMYQFTVLGQR
WYLANFSHATSFNFTTREQVPVCLDLYPTTDYTVNVTLLRSPKRHSVQIT IATPPAVKQTI
SNISGFNETCLRWSIKTADMEEMYL FHIWGQRWYQKEFAQEMTFNIISSSSRDPEVCLDLRP
GTNYNVSLRALSSEL PVVISLTTQITEPPLPEVEFFT VHRGPLPRLRLRKAKEKNGPISSYQ
VLVLPLALQSTFSCDSEGASSFFSNASDADGYVAAELLA KDVPDDAMEIPIGDRLYYGEYYN
APLKRGS DYCIILRITSEWNKVRRHSCAVWAQVKDSSLMLLQ MAGVGLGSLAVVIILTFLSF
SAV
```

Important features of the protein:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 718-740

N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352, 367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474, 498-502, 503-507, 542-546, 563-567, 645-649

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

Tyrosine kinase phosphorylation site.

amino acids 419-427

N-myristoylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126,
146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694,
727-733.

Amidation site.

amino acids 52-56

Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

Cytochrome c family heme-binding site signature.

amino acids 39-45

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 85-106, 135-156

Receptor tyrosine kinase class V proteins:

amino acids 389-422

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTG
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTACAAACATCGAG
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
CTGACTCCACTGAAGCAAACACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTCAGCAGTGGGCAAACAACCTTC
CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC
GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCCACGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
TTAAATTTCACTCAGTGTGGCCCAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722

><subunit 1 of 1, 482 aa, 1 stop

><MW: 49060, pI: 4.74, NX(S/T): 4

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAIFDTLCTDDSSSEEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVETPSY
 VKVSGAAPVVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRRLPGRGRPQT

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
 314-320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAG
GCCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCA
GGCAGTCCAATTTCAAGAATATGTCTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
CCCAGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCA
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT
ACTTCGCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA
ACTGGCTCTGTTCTGTTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
AAATGTTTGTGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT
GTAGCTAAGGATTGGAATGACAACCCCCGGAAAAATTTTCGGGTATTCTGAGATACTGGT
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
GCTCCCTTCATGCTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCTTCTCGG
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCA
GCTATTCATTAACCTCCGGGACCTGGGTGGCACAAGTGGATCATTGCCCCCAAGGGGTTC
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT
TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGGTAGGATGTCAAGAAATGGGAAT
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTA
GATCGAAATGTC

FIGURE 36

MLRFLPDLAFSFLILALGQAVQFQYVFLQFLGLDKAPSPQKFQVPYILKKIFQDREAAA
TTGVSRLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTPKPGKMFVLRVWPWPQGAVHFNLLDV
AKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK
RRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPHGECPFSLTISLNSSNY
AFMQALMHAVDPEIPQAVCIPTKLSPISMYQDNNDNVILRHYEDMVVDECGCG

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

CACCTTCTCCCTCTCTTCTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTTCGACAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCCTTGGCTCTGGCCTGGT
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCA
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCGCTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTTACC GGCAAGTTCTACTGCTAC
GTGCCCGGCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC
CCTGGCTTTGGCATTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
GAGACGCGGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGGCTCCAGTCTTTGAAATA
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCGGGGGCAGG
AAACTACCTCTGGCTTAATTCTTTTAAAGCCACGTAGGAACCTTTCTTGAGGGATAGGTGGAC
CTGACATCCCTGTGGCCCTTGCCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCGAGGT
TAGGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCACAGACCCTGGGGGGTGGTCTCCATGCCTGCCACCCTGGCATCGGCT
TTCTGTGCGCCTCCACACAAATCAGCCCCAGAAGGCCCGGGCCTTGGCTTCTGTTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCCACTGCCCT
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTTGCTGTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATTCACTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCACAGACTCTGATCTCCAGGAACCC
ATAGCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC
CCCAAACCCCCGCTGCCTCTCTTCCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC
TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCAAGCTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDGRGLQGKYGKTGSAGARGH
TGPKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGAC**ATGG**CTG
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCCTGT
GACACTCAAGAGCTACGATGTCTGTGTATTCAAGGAACACTCTGAATTCATTCCTCTCAAAC
CATTAAAAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG
TCCCCAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT
GGCCCAATTACTAACAGGTTTCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT
GAAGCTTCTGTATAGTGTTGAGCATGAAAAGCCTCTATATCTTTCAATTTGGGAGACCTGAGA
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCC**TA**
AAAGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTTGGCGTTCTCA
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
TATTATAAATGTTTTATTTACTTAACTTCCTAGTGAATGTTACAGGTGACTGCTCCCCCAT
CCCCATTTCTTGATATTACATATAATGGCATCATATACCCCTTTATTGACTGACAACTACT
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
TGCATCTCGGTGTAGAGCAAGGCTCCTTGTCTTCAGTGCCCCAGGGTGAAATACTTCTTTGA
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
```

```
><subunit 1 of 1, 167 aa, 1 stop
```

><MW: 19091, pI: 7.48, NX(S/T): 1

MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIKNIIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPAMPKLLYSVEHEKPLYLSFGR
PENKRIFFPPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

FIGURE 41

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG
CTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCATAGCCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACACAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGGAGAGTCTCCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCCT
TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCNCCA

FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLILVLAFGIPRTQGS DGGAQDCCLKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPAQGCRKDRGASKTGKKGKGSKGCKR
TERSQTPKGP

Important features of the protein:**Signal peptide:**

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATG**AAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSEFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

GCTCCCGAGCCAAGAACCCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCTGGCCG
CTAAGCGAGGCCCTACCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCCCGGGCCCGGGAGGGGGGCTGGGGCTGGGGCCGAGAGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGAG
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTTGCATCCGTGCCGACGGCGCTCGTGGACTGCGCGCGGGGC
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGGCCACTTGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTTAACT
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCGTCTGCTTGAATACCTCCATCGATGGGGAAC
TCATTCTCTTTGGAAAAATTTATATGTCAAGCTGAAATTTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTATTTTAATTTAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAATGACTGGAGCAGGCATGGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGC
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAAATGGAGTTTGT

FIGURE 46

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPRLRLHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFKEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 47

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
 GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
 CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
 GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
 AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
 TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
 ACTTGATATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
 GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
 CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
 GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
 GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCGTGTCAGCCTCTGATACTGGAGAATACA
 GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
 GTGGAGCGGAATGTGGGGGTCATCGTGGCAGCCGTCTTGTAAACCCTGATTCTCCTGGGAAT
 CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
 CTTGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCCGAAGTGAAGGAGAATTCAAACAG
 ACCTCGTCATTCTGCTGGTTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
 CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTTACAGGATGCCTTATTTGTCTTC
 TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
 ATCCTCCTTCATGCCCTCCCTCCCTTTCTACCCTGCTGAGTGGCCTGGAACCTGTTTTAA
 GTGTTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
 TTCTAAGTAGACAGCAAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACCTGGC
 TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
 GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGGCTAGAGCGGCTGAAATGGTTGTTTG
 TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
 CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
 GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAG
 GATTTAAACCGCTGCTCTAAAGAAAAGAAAAGTGGAGGCTGGGCGCAGTGGCTCACGCCTG
 TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA
 ACATGGAGAAACCTACTGGAATAACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
 CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTRRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 49

CCCACGCGTCCGAACCTCTCCAGCG**ATG**GGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAACATAACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTACG**TAG**TCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCCGCCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTCACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTTTGTTTGTTTGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCCTGC

FIGURE 50

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLE
NNYTAFQONARHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

GTTGTGTCCTTCAGCAAAAACAGTGGATTTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
 TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA
 AAAAAAATC**ATG**AAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
 GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
 CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
 GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
 CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
 AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
 CACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT
 TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
 CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
 GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
 CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA
 TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
 TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
 GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
 AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
 ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
 CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTT**TGA**TGTGAGTGCC
 ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACAAACAGCAATGGCAACAC
 CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
 AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAGAAATTGAA
 AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
 ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
 GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
 AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCCAAGCGTGGCGCTGCGG
 GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
 AAAAA

FIGURE 52

MKTIQPKMHNSISWAI FTGLAALCLFQGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTQLQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHGTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Signal peptide:

amino acids 1-28

FIGURE 53

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAG**ATG**
 AAGTTCCAGGGGGCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
 CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC
 TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCA
 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAACTTCTGG
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG
 GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCCTGGGGA
 TCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACC
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCAGGGCTTCA
 GAGGACAGGGAGTTTCCAGCAACATGAGGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGGG
 GGCTCTGGAGACAATTATCGGGGGCAAGGGTTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCT
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA
 AGCTCTCGCATCCCC**TGA**CCCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCAGACT
 CCCTCCTTAAAACACCACCCTCTCATCTACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTA
 GCTGCCCCACAAA
 AA

FIGURE 54

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
```

```
><subunit 1 of 1, 440 aa, 1 stop
```

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEG VGKAIGKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGQGNPGGLGTPWVHGYPGNSAGSFGM
 NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
 GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSGGSSGGSSGGSSGNSGGSRGDSGSESSW
 GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
 GSGDNYRGQGSWSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC
AAATGCAACGCCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

FIGURE 58

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGESS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGGCAACACAGGCTGATAAGACACAGAGCAGCGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGGCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGCGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCTCT
GAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTC
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
TGGATTTCTCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
AATATTAGACCATTTTACGGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC
TCAAATTTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCTATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
CACCCCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGTATAATCTCTCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA
ATATATCCCTTCATCTCTCAACCTTGCGGGTTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG
GGATGGCCGTCAGGGAATTAATATGAATCTTTTGTCTGTCCACCACGACCCCGGCTCTG
CCTCTCTTCACCCAGCCCCAAGTACAGCTTCTCCGACCATCCAGCTCCCACCTCTCTAT
TCCAAACCTTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAAGAGC
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC
CCAGAAGTGGAATACAACCGGGGCCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCCTTAAATAACGAT
CAACTCCTTAAAGGAGATTTTCAAGTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTTATACGGTGTACTATATAATGGGATTTTAAAAAAGTG
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACTCTTTTGCTTTTTTAAATCTT

FIGURE 60

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
 SRAALAQLLKLEELHLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTTPGLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
 DFRLLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
 522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCA**ATG**AACTGTTATTTACTGCTGCGTTT
 TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
 AAGTCAAGCAGCCAGTGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
 TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
 CAATGGAAACAATTCCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
 TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
 TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
 GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG
 AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
 GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
 ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
 TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
 TCTGGAACAACAAGTGTATTAATTAACTTTTCAGATGTTAATGACAATAAGCCTATATTTAA
 AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
 GATTGCGAAACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTTAAA
 AAAGAAAGTGGATTTTGGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCATC
 ATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTTCATTAAGATCCAG
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA
 AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
 CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC
 ACTACAAGTAACCTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
 AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAACATCA
 ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
 GGTCAGGTAAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
 TTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTACAATCATAGATAATCAAG
 ATAACACAGCTGTCAATTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
 TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
 CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
 TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATA
 TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCTGA
 GAAAAGTGAAGATTTTCAGAGAGAATATATTTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
 ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
 CGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
 CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
 CCCCTCCTTTTGAATTCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC
 CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
 GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAAT**TAGG**
 GCTTTTTACCATCAAAATTTTTAAAAGTGCTAATGTGTATTTCGAACCCAATGGTAGTCTTAA
 AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
 CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCTATTGAACAGAGATGTG
 GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG
 TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
 CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
 CAAGTCAAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
 ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT
 TTAA

1002796
 24501

FIGURE 62

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKGWVWNQFFVPEEMNTTSHH
 IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
 GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
 LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
 VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
 TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
 PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
 WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
 DESIEEHFHYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
 SLTSTNTLTIHVCD CGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
 RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
 RQSLQVGPDSAIFRKFILEKLEEANTDPCAPFPDSLQTYAFEGTGS LAGSLSSLES AVSDQD
 ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGC
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGAC
AAGTCCAACCTTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTC
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAGGAAGATGGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
TAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185

><subunit 1 of 1, 179 aa, 1 stop

><MW: 20011, pI: 8.10, NX(S/T): 3

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLF PQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCTCCGGCTGCGAGAAAGGA
 CGCGCGCCCTGCGTCGGGGCGAAGAAAAGAAGCAAACTTGTCTGGGAGGGTTTCGTCATCAAC
 CTCCTTCCCCGCAAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCA
 GAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGCGCTGGCTGTGGAATTAGATCTGT
 TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGCACCGGGTTGG
 CGCTGCCCCGAGTGGAAACCGACAGTTTGGGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCG
 GTTGTGTTGAGTGTCTGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGG
 TCCGAAGAGCGCTGCGCTCCTACTCGCGTTTCGCTTCTTCTCCTCTTCTCGGTTCCTACTGTGA
 AATCGCAGCGACATTTACAAAGGCCTCCGGGTCTACCGAGACCGATCCGCAGCGTTTGGCC
 CGGTGCTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAAATGCGGAGGTTCCCAGAGGC
 CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTCACGGACCAAGTTTCAGTTTCG
 CCGATGGGAAACCCGGAGACCAAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT
 CACACAGAGGAGGAGGTGGAAGTTGATTACACGCGTACAGCCACAGGTGGAAAAGAACTT
 GGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGAGCCCA
 GAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT
 ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTT
 ATGGGTGAACATAGACCAAATGGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATA
 CTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGCCACTTCCTA
 CGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGTCGTACATCGAATGCT
 AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCAGTGTATCCAGAAATT
 CAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTC
 CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCCTGCTCATGGATGGACGAAT
 CATCTTTGGATACAAAGAAATTCCTGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAG
 TGAAAGTCGGACTGTCCGATGCATTTGTCGTTGTCCACAGGATCCAACAAATTCCCAATGTT
 CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTACCAACAT
 TTCGGCTGTGGAGATGACCCCATTAACCCACATGCCTCCAGTTTAACAGATGTGGCCCCCTGTG
 TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGGA
 TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGAT
 GTGTGAGAATACAGAACCAGTGGAACTTCTTCTCGAACCACCACAACCGTAGGAGCGACAA
 CCACCCAGTTCAGGGTCCTAACTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCCACCAGC
 CTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA
 TGACAGTGCAGCTGAGAAGAAAGGGGAACCTCCACGCTGGCCTCATCATTGGAATCCTCA
 TCCTGGTCTCTATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACA
 TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAG
 AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACCAGTTGGAGAGAAAGAAGGCTTTA
 TTGTATCAGAGCAGTGCTTAAATTTCTAGGACAGAACAACACCAGTACTGGTTTACAGGTGT
 TAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACAAACACACACAAACAAGCTC
 TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGG
 TAAACAAAAAACTAAACTTATACAAGATACCATTTACTGAACATAGAATTCCTTAGTGG
 AATGTCATCTATAGTTCCTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA
 TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAAATCATAATAAAGC
 TTTAGTTCATGAGGG

FIGURE 66

MARFPKADLAAAGVMLLCHFFFTDQFQFADGKPGDQILDWQYGVTAFFPHTEEEVEVDSHAYS
HRWKRNLDFLKAVDTNRRASVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYIISRIYGPS
DSASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTG
EUVHRMLTATQYIAPLMANFDPSSVRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT
LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRTIYEHVELQ
MSKITNISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCP
EESKEKMCENTEPVETSSRTTTTVGATTTQFRVLTTTTRAVTSQFPTSLPTEDDTKIALHLK
DNGASTDDSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSR
WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

FIGURE 67A

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGCTTGTTCGTAACCAAGTG
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCTCCTGCCTCCCGGTGGACAGA
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTG
CTTAGGTGTTATTTGGAAGATGGAGCTTCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTAT
TTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTGTTCT
GTTTCAGACTCAACATACACCCAGAACAATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAA
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCCATCAGCAAAACCA
TTTGAAAATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA
ATGCAGTGCAGAAAATGATGTGTCATTCCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACT
TTGCTCCTACTATTCAGGAAATTAATCTGGCACCGTGACCCCCGGACGCAGTGGCCTGATA
AGATGTGAAGGTGCAGGTGTGCCGCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT
CTTCAATGGCCAACAAGGAATTATTATTCAAATTTTAGCACAAGATCCATTCTCACTGTTA
CCAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACA
ACCAATGCGAGCCTGCCTCTTAACCTCCAAGTACAGCCAGTATGGAATTACCGGGAGCGC
TGATGTTCTTTTCTCCTGCTGGTACCTTGTGTTGACACTGTCCTCTTTCACCAGCATATTCT
ACCTGAAGAATGCCATTCTACAATTAAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCT
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAAGCAGCGTGGGATATAATC
AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAAT
TCTACTCTTTTTTGTATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAG
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAACTAC
AACTTTTCAAAGCATTTCAGTCATGGTCTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAA
TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTTCCTGTTTCAAT
AAGAGTCAATCCACATTTACAAAGATGCATTTTTTTTCTTTTTTGATAAAAAAGCAAATAATA
TTGCCTTCAGATTATTTCTTCAAATATAACACATATCTAGATTTTTCTGCTCGCATGATAT
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTTCCTGT
AAGTTCAGCATGGGTGTGCCTTCATACAATAATATTTTTCTCTTTGTCTCCAATAATATAA
AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCAAGAGTGATCAAGTTAAACCA
TACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCTGCACTGACAA
TGGGGTTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAAC
AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
AATCATTTCCCTTTAAAATGACAGCACAGTCCACTCAAAGGATTGCCTAGCAATACAGCATCT
TTTCCTTTCACTAGTCCAAGCCAAAAATTTTAAGATGATTTGTCAGAAAGGGCACAAAGTCC
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTAATTTTATTTTGTGGCAGCTAA
GTTAGTATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA
GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAAATATATTA
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTCTTCAATAA
AATCTTTCTATATAGCCATTTTCAGTGCAAACAAGTAAAATCAAAAAAGACCATCCTTTATTT
TTCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAATAT
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAA
AACTACATTTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG
TTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTT
ACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCCTTTTACAAGTTGTAACAACAAAG
ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAG
TATGTTGCCCTAGCAGGGATGGCTTAAAACTGTGATTTTTTTTTCTTCAAGTAAAACTTAGT
CCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAAT
AAATGTATGACATTATTTTGATTGATACATTAAAAAGAGTTTTTTAGAACAAATATGGCATT
TAACTTTATTATTTATTTGCTTTTAAGAAATATTCTTTGTGGAATTGTTGAATAAACTATAA
AATATTATTTTGTATTGCAGCTTTAAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

AGTGGTGCTACCAACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT
TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAAATAATTAGTTCAAAGTGTTGTCATG
ATTCCAAATTTGTGGAGTCTGGTGTTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTTCTTGAGTGACATTTTTTAAATA
GAGGAGGTATTCACTATGTTTTTCTGTATCACAGCAGCATTCCCTAGTCCTTAGGCCCTCGGA
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTTCAGAATAG
CAGTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCATTTTCAGG
ANTATATTTTCTACAAGTTCCTACTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTTAAAG
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAAGAAAAAGAAATG
AAAAGGAAAGGCAGTAAAGAGGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGGAAGGAAGAATCAGAGTATTAGG
GTAGTTAACTTACACATTTGCATTCTTAGTTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAGTTCCTATTATGCAGCAATTATAT
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGGAGACACTAAAAGATTTGAG
AGGGAGAATTTCAAAGTTAAAGCCACTTTTGGGGGGTTTATAAGTAACTGAAAAATTAATG
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGGAACTGAGAAAATTACCCAG
GTAATTCAGGGGAAAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTTCA
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
GATTCCTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
CATCCATATTTTCATAACCTGATGTAAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC
TCAGTTTTATCAATTAA

FIGURE 68

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259

><subunit 1 of 1, 354 aa, 1 stop

><MW: 38719, pI: 6.12, NX(S/T): 6

MDMMLLVQGACCSNQWLA AVL LSLCCLLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYL
 EDGASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKR DYS LQIQNV DVTDDGPYTCSVQTQH
 TPRTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQ
 YLDIYGITRDQAGEYECSAENDVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGA
 GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASL
 PLNPPSTAQYGITGSADVLFSCWYLVLTLSFTSIFYLKNAILO

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.

amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
 304-310, 321-327

Myelin P0 protein.

amino acids 94-123

FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACA
ATTTACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTG
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
TTAATTAAGGGGTTACATCCAACCCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGAC**ATG**TATAGACACAAAAA
CAGCTGGAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAA
CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
GCCCACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC
CGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAG
GCCAGTGCCGGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC
ACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCT
TCTCCTCCTGCAAA**TAG**

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175

><subunit 1 of 1, 155 aa, 1 stop

><MW: 17194, pI: 10.44, NX(S/T): 0

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features of the protein:**Transmembrane domain:**

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATG**GCGTGGAGCCTTGGGA
GCTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTC
AGAATGAATTCTGTAAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG
GAACCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA
CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
AGGGCTGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGA
CACCATTATTGGACCCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT
TCTTAGCCCCCTAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCA
TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA
GTATGACTTTGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAAGTTGAG
GGTTTCTTCCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACC
CATGACGAAACGGTCCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGT
CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCGTTTACAAGAAGACAAAGTACG
CCTTCTCCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
AACACACTTCTGTTTTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAG
TGTCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
CCCCGCTGGGCAGGGGGCCCCAAAGCT**TAG**GCTCTGAGAAGGAAACACACTCGGCTGGGCACA
GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGA
CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
TTTAAAGGCTGTCTTGGCAAAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCA
TGATGTTTTTCAAGATTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAA
GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCA
CCTTAGAGGTCGAGGCAGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATA
TGGTGAAACCCAGTCTCTACTAAAAATACAAAATTAGCTAGGCATGATGGCGCATGCCTAT
AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
GGTTGCAGTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT
CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAATGAGGAATAAGAATGG
AGATGTTACATCTGGTAGATGTAACATTCTACCAGATTATGGATGGACTGATCTGAAAATCG
ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGATTCTTTGCA
GTACTTTGAATTTATTTTTCTACCTATATATGTTTTATATGCTGCTGGTGCTCCATTAAAGT
TTTACTCTGTGTTGC

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551

><subunit 1 of 1, 325 aa, 1 stop

><MW: 37011, pI: 5.09, NX(S/T): 4

MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTT
YCVQVRGFLPDRNKAGEWSEPVCQTTHDETVPSWMVAVILMASVFMVCLALLGCFSLLWCV
YKKTKYAFSPRNSLPQHLKEFLGHPHHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPG
DSCSLGTTPPGQGPQS

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCCGCTCGCCGCCCGCC**ATG**GCCC
GCGCAGCCCCGCTGCTCGCCGCGTTGACCCGCGTCTCTCGCCGCCCGCGCTGCTGGCGGAGAT
GCCCCGCCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATT
TCTCCAGCAGCACTTTTGACCTCGGGTGCAGATCGACGTGTACGAGAAGGGAACCGTGGGTG
GCCGCTTGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCTCCTTCCAC
TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT
GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACG
TGCTGAACCTCTTCCGCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG
GTGGAGGAGGTGATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT
CTCGGGTGTGGAGGAGCTGCTCTACTACTGGGGGAGTCCACCTTTGTTAACATGACCCAGC
ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTTATTGATGATGTGCTT
TCTGCTGTCTTGCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCCTTTGCAGGAGCCAT
GTCCTAGCCGGGGGCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTTTGT
CCGTTTTGCTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCCTG
CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC
TGACTTCTATGACATCGTGGTCATCGCCACCCCCCTGCACCTGGACAACAGCAGCAACT
TAACCTTTGCAGGCTTCCACCCGCCATTGATGACGTGCAGGGCTCTTTCCAGCCCACCGTC
GTCTCCTTTGGTCCACGGCTACCTCAACTCGTCTACTTCGGTTTCCAGACCCTAAGCTTTT
CCCCTTTGCCAACATCCTTACCACAGATTTCCCCAGCTTCTTCTGCACTCTGGACAACATCT
GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTGGCGA
GTCCAGTCCCCCAAGCCCCCTCTTTCGGACCCAGCTAAAGACCCTGTTCCGTTCCCTATTACTC
AGTGCAGACAGCTGAGTGGCAGGCCCATCCCCCTCTATGGCTCCCGCCCCACGCTCCCGAGGT
TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGGCGGCCAGCTCCGTGGAG
GTGATGGCCGTGGCTGCCAAGAAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT
AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAACTGTGAGGGCTCTAGG
GAGAGCCTGGGAACCTTTCATCCCCCACTGAAGATGGATCATCCCACAGCAGCCCAGGACTGA
ATAAGCCATGCTCGCCACCAGGCTTCTTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
ACCTACTGTCTGCCTATATTAAGGGTCCACACGGCGCTGCTGCTTTTTTTTTAAGGGGGAAA
GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTTATTTATTTTTTTTTAAGAAGAA
AAAAGTTCATCTTCACAAGGTGCTTCAGACTTGGTTTTCTTAGCTAGAAACCAGAAGACTACG
GGAGGGAATATAAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCACTACCTACTC
CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAACCAGATGGTTACAAA
TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGGACT
TGATGGATTTGAAGTACCTAGTTCAGAAGTCCCTAGTCACCATCTCCAAGCCTGTCAACATC
ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAAGGAAGAGATGTGTGCCTGAATAGTC
GTCACCATATCTCCAAGCTTCCTGGCAACCAGTGGGAAAAGAAACATGCGAGGCTGTAGGAA
GAGGGAAGCTCTTCCTTGGCACCTAGAGGAATTAGCCATTCTCTTCCTTATGCAAAGATTGA
GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTCATATCTTACCCC
TAGATGTTTCATCCCAGCAGAAGAAAGAAGAGGTGTTGGGGTAGGATTCTTCAGAGGTTAGC
CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT
TTCTACAAACCCTTAAAAATCACTTGTTTTAAAAAGAAAGTAAAGCCCTTTTCATTCAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510

><subunit 1 of 1, 494 aa, 1 stop

><MW: 54646, pI: 7.27, NX(S/T): 6

MARAAPLLAALTALLAAAAAGGDAPPGKIAVVGAGIGGSAVAHFLQQHFGPRVQIDVYEKGT
VGGRLATISV NKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTQRFIDDVSAVLRASYGQSAAMPAFAGAMSLAGAQQGSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVS LVHGYLNSSYFGFPDPKLFPPFANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEA AVWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPLYGSRPTL
PRFALHDQLFYLNLEWAASSVEVMAVA AKNVALLAYNRWYQDL DKIDQKDLMHKVKTEL

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435